

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 / Search time 40.9396 Seconds

(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-2

Perfect score: 3619
Sequence: 1 MAPITVAQAQTRGLGCLIT.....PAIIPDREVLVREFDMEEC 686

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3619	100.0	686	5 AAU76377	Aau76377 Hepatitis
2	3619	100.0	686	5 AAE18689	Aae18689 HCV-1 NS3
3	3619	100.0	686	6 ABG72261	Abg72261 HCV-1 NS3
4	3619	100.0	686	7 ADC06767	Adc06767 HCV mutan
5	3602	99.5	2261	1 AAP90164	Aap90164 Peptide e
6	3602	99.5	2436	1 AAP92050	Aap92050 Sequence
7	3602	99.5	2436	1 AAP92058	Aap92058 Peptide e
8	3602	99.5	2772	3 AAB18540	Aab18540 Protein e
9	3602	99.5	2955	2 AAY14975	Aay14975 Amino aci
10	3602	99.5	2955	3 AAB18541	Aab18541 Polypept
11	3602	99.5	3011	2 AAP90931	Aap90931 Hepatitis
12	3602	99.5	3011	2 AAM44480	Aam44480 HCV polyp
13	3602	99.5	3011	2 AAM40038	Aam40038 HCV polyp
14	3602	99.5	3011	5 AAE22049	Aae22049 Hepatitis
15	3600	99.5	728	5 AAE18688	Aae18688 NS3/aa mu
16	3600	99.5	728	7 ADC06766	Adc06766 HCV mutan
17	3599	99.4	2301	1 AAP92047	Aap92047 Sequence
18	3594	99.3	2772	2 AAR08123	Aar08123 Hepatitis
19	3594	99.3	686	4 AAB62633	Aab62633 HCV NS3/4
20	3593	99.3	3011	2 AAR21519	Aar21519 Compiled
21	3590	99.2	3011	2 AAR21515	Aar21515 HCV polyp
22	3589	99.2	3011	2 AAR31621	Aar31621 Hepatitis
23	3587	99.1	3011	5 AAU84597	Aau84597 HCV polyp
24	3586	99.1	2816	2 AAR34009	Aar34009 HCV-1 pol
25	3583	99.0	1786	1 AAP90158	Aap90158 Protein s

26	3583	99.0	2436	2 AAR28582	Aar28582 HCV amino
27	3583	99.0	2894	2 AAR70230	Aar70230 Composite
28	3580	98.9	2894	2 AAR24440	Aar24440 Composite
29	3579	98.9	1766	1 AAP92041	Aap92041 Hepatitis
30	3565	98.5	686	5 AAE21837	Aae21837 Hepatitis
31	3565	98.5	686	5 AAE19900	Aae19900 Hepatitis
32	3565	98.5	686	7 AEW00351	Aew00351 Hepatitis
33	3561	98.4	686	5 AAE21838	Aae21838 Hepatitis
34	3561	98.4	686	5 AAE19907	Aae19907 Hepatitis
35	3561	98.4	686	7 AEW00358	Aew00358 Hepatitis
36	3560	98.4	3011	2 AAR40120	Aar40120 HCV genom
37	3560	98.4	686	5 AAE21840	Aae21840 Hepatitis
38	3560	98.4	686	5 AAE19919	Aae19919 Hepatitis
39	3560	98.4	686	7 AEW00370	Aew00370 Hepatitis
40	3560	98.4	2955	2 AAR08124	Aar08124 Hepatitis
41	3560	98.4	3011	2 AAW77397	Aaw77397 Hepatitis
42	3560	98.4	3011	6 ABP71460	Abp71460 Amino aci
43	3560	98.4	3012	5 AAU92829	Aau92829 Hepatitis
44	3560	98.4	3012	6 ABU61848	Abu61848 HCV H77 C
45	3559	98.3	686	5 AAE21843	Aae21843 Hepatitis

ALIGNMENTS

RESULT 1

ID AAU76377 standard; protein; 686 AA.

AC AAU76377;

DT 08-MAY-2002 (first entry)

DE Hepatitis C virus NS3/4a conformational epitope protein sequence.

KM Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;

KW immunoassay solid support; multiple epitope fusion antigen; MEPA;

KW non-structural protein; mutant; mutein.

XX Hepatitis C virus.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 403 /note= "Wild-type Thr substituted by Pro"

FT Misc-difference 404 /note= "Wild-type Ser substituted by Ile"

FT WO200196870-A2.

PD 20-DEC-2001.

PN 14-JUN-2001; 2001WC-US019156.

PF 15-JUN-2000; 2000US-0212082P.

PR 02-APR-2001; 2001US-0280811P.

PR 02-APR-2001; 2001US-0280867P.

XX (CHIR) CHIRON CORP.

PA Chien DY, Arcangel P, Tandestre L, George-Nascimento C, Coit D;

PI Medina-Selby A;

DR WPI; 2002-090228/12.

DR N-PSDB; ABK15344.

PT Immunoassay solid support, useful for detecting hepatitis C virus

PT infection in biological sample; comprises HCV NS3/4a conformational

PT epitope and multiple epitope fusion antigen bound to the support.

PS Claim 5; Fig 3; 92pp; English.

XX The present invention relates to a new immunoassay solid support

see ID NO. 2

CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
CC conformational epitope and a multiple epitope fusion antigen (MEPA),
CC bound to the support. The NS3/4a conformational epitope and/or MEPA
CC reacts specifically with anti-HCV antibodies present in a biological
CC sample from an HCV-infected individual. The immunoassay of the invention
CC is useful for detecting hepatitis C virus infection in a biological
CC sample. The method of the invention provides a sensitive, accurate
CC diagnostic and prognostic tool to provide adequate patient care and to
CC prevent transmission of HCV by blood and by blood products, or by
CC personal contact. Use of NS3/4a conformational epitope in combination
CC with MEPA, provides a sensitive and reliable method for detecting early
CC HCV seroconversion. Use of MEPA has the added advantages of decreasing
CC masking problems, improving sensitivity in detecting antibodies by
CC allowing a greater number of epitopes on a unit surface area of
CC substrate, and improving substrate. Detection accuracy is increased and
CC the incidence of false results is reduced because of the identification
CC and the use of highly immunogenic HCV antigens which are present during
CC the early stages of HCV seroconversion. The present amino acid sequence
CC represents the non-structural protein NS3/4a conformational epitope of
CC the invention
XX

SQ Sequence 686 AA:

Query Match 100.0%; Score 3619; DB 5; Length 686;

Best Local Similarity 100.0%; Pred. No. 1.6e-306;

Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAPITAAOQTRGLGCIITSLTGRDNQVEGEVOIVSTAOTFLATCINGVCTVYHGA 60
1 MAPITAAOQTRGLGCIITSLTGRDNQVEGEVOIVSTAOTFLATCINGVCTVYHGA 60
61 GTRITASPCKGVIOYNTNVDDLVGMPAPQSGRSILPTCTGSSDLYLTRADVIPIVRR 120
61 GTRITASPCKGVIOYNTNVDDLVGMPAPQSGRSILPTCTGSSDLYLTRADVIPIVRR 120
61 GTRITASPCKGVIOYNTNVDDLVGMPAPQSGRSILPTCTGSSDLYLTRADVIPIVRR 120
121 GDSRGSILSPRPISYLKSSGGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
121 GDSRGSILSPRPISYLKSSGGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
121 GDSRGSILSPRPISYLKSSGGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
181 RSPVFTNDSPPVPOSFVHHAHPGSGSTVPAVAOQKVLVANSVAATLGF 240
181 RSPVFTNDSPPVPOSFVHHAHPGSGSTVPAVAOQKVLVANSVAATLGF 240
181 RSPVFTNDSPPVPOSFVHHAHPGSGSTVPAVAOQKVLVANSVAATLGF 240
181 RSPVFTNDSPPVPOSFVHHAHPGSGSTVPAVAOQKVLVANSVAATLGF 240
241 AYMSKAGHIDNIRITGRTITTSPTITSTYTGKFLADGCGGAVDIIICDECHSTATS 300
241 AYMSKAGHIDNIRITGRTITTSPTITSTYTGKFLADGCGGAVDIIICDECHSTATS 300
241 AYMSKAGHIDNIRITGRTITTSPTITSTYTGKFLADGCGGAVDIIICDECHSTATS 300
241 AYMSKAGHIDNIRITGRTITTSPTITSTYTGKFLADGCGGAVDIIICDECHSTATS 300
301 ILGIGTVLDDAETAGARLVLAATPPGSAVTPHPNIEVALSTGELIPFGAKAIPLEVI 360
301 ILGIGTVLDDAETAGARLVLAATPPGSAVTPHPNIEVALSTGELIPFGAKAIPLEVI 360
301 ILGIGTVLDDAETAGARLVLAATPPGSAVTPHPNIEVALSTGELIPFGAKAIPLEVI 360
361 KGGHILFCHSKKCCDELAALVALGINAVYRGLDVSVIPIGDVVVAATDMLMGYT 420
361 KGGHILFCHSKKCCDELAALVALGINAVYRGLDVSVIPIGDVVVAATDMLMGYT 420
361 KGGHILFCHSKKCCDELAALVALGINAVYRGLDVSVIPIGDVVVAATDMLMGYT 420
421 GDFPSVIDCNCVTQTVDFSLDPTFTIETITLPODAVSRTORGRGTGKGIYFVPA 480
421 GDFPSVIDCNCVTQTVDFSLDPTFTIETITLPODAVSRTORGRGTGKGIYFVPA 480
421 GDFPSVIDCNCVTQTVDFSLDPTFTIETITLPODAVSRTORGRGTGKGIYFVPA 480
481 ERPSGMEPSSVLCCEYDAGCAWELTPAETTVRLAAMNTGQLPVCOHLEFWEVVFGL 540
481 ERPSGMEPSSVLCCEYDAGCAWELTPAETTVRLAAMNTGQLPVCOHLEFWEVVFGL 540
481 ERPSGMEPSSVLCCEYDAGCAWELTPAETTVRLAAMNTGQLPVCOHLEFWEVVFGL 540
541 THIDHNFISORTKOSGENPYLVAQATVCARAOAPPSMDOMKCLILKFTLHGPFTLL 600
541 THIDHNFISORTKOSGENPYLVAQATVCARAOAPPSMDOMKCLILKFTLHGPFTLL 600
541 THIDHNFISORTKOSGENPYLVAQATVCARAOAPPSMDOMKCLILKFTLHGPFTLL 600
601 YRLGAVONEITLTHPTVKITMTCSADLEVVTSTWLVGVLAALAAVCLSTGCVVIYGR 660
601 YRLGAVONEITLTHPTVKITMTCSADLEVVTSTWLVGVLAALAAVCLSTGCVVIYGR 660
601 YRLGAVONEITLTHPTVKITMTCSADLEVVTSTWLVGVLAALAAVCLSTGCVVIYGR 660
661 VTLGKPAIIPREVLYRPFDEMEBC 686
661 VTLGKPAIIPREVLYRPFDEMEBC 686

Db 661 VTLGKPAIIPREVLYRPFDEMEBC 686

RESULT 2

AAE18689

AAE18689 standard; protein; 686 AA.

XX

AC

17-MAY-2002 (first entry)

XX

HCV-1 NS3/4a mutant conformational antigen.

XX

Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutein.

XX

Hepatitis C virus type 1.

OS

XX

Key

Location/Qualifiers

FH

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Query Match 100.0%; Score 3619; DB 5; Length 686;

Best Local Similarity 100.0%; Pred. No. 1.6e-306;

Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAPITAAOQTRGLGCIITSLTGRDNQVEGEVOIVSTAOTFLATCINGVCTVYHGA 60
1 MAPITAAOQTRGLGCIITSLTGRDNQVEGEVOIVSTAOTFLATCINGVCTVYHGA 60
61 GTRITASPCKGVIOYNTNVDDLVGMPAPQSGRSILPTCTGSSDLYLTRADVIPIVRR 120
61 GTRITASPCKGVIOYNTNVDDLVGMPAPQSGRSILPTCTGSSDLYLTRADVIPIVRR 120
61 GTRITASPCKGVIOYNTNVDDLVGMPAPQSGRSILPTCTGSSDLYLTRADVIPIVRR 120
121 GDSRGSILSPRPISYLKSSGGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
121 GDSRGSILSPRPISYLKSSGGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180
121 GDSRGSILSPRPISYLKSSGGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETTM 180

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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 49.4736 Seconds

(Without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-4

Sequence: 1 MATRAVCVTKGDPVQGIIN.....GNKDRSTGKSGKRGYPWP 829

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

- 1: geneeqp1980s:*
- 2: geneeqp1980s:*
- 3: geneeqp2000s:*
- 4: geneeqp2000s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4455	100.0	829	5	AAE18690 Multiple
2	4455	100.0	829	7	ADCO6769 Chimeric
3	4032	90.5	1099	5	AAU76378 HCV multi
4	4032	90.5	1099	6	ABG72262 HCV multi
5	2222	49.9	1021	2	AAW34481 HCV anti
6	2222	49.9	1021	5	AAW40039 Fusion pr
7	2222	49.9	1021	5	AAE22050 pSOD/c200
8	1627.5	36.5	1766	1	AAE22050 pSOD/c200
9	1624.5	36.5	2261	1	AAE22050 pSOD/c200
10	1624.5	36.5	2261	1	AAE22050 pSOD/c200
11	1624.5	36.5	2261	1	AAE22050 pSOD/c200
12	1624.5	36.5	2261	1	AAE22050 pSOD/c200
13	1624.5	36.5	2261	1	AAE22050 pSOD/c200
14	1624.5	36.5	2261	1	AAE22050 pSOD/c200
15	1624.5	36.5	2261	1	AAE22050 pSOD/c200
16	1624.5	36.5	2261	1	AAE22050 pSOD/c200
17	1624.5	36.5	2261	1	AAE22050 pSOD/c200
18	1624.5	36.5	2261	1	AAE22050 pSOD/c200
19	1624.5	36.5	2261	1	AAE22050 pSOD/c200
20	1624.5	36.5	2261	1	AAE22050 pSOD/c200
21	1623	36.4	781	2	AAE22050 pSOD/c200
22	1623	36.4	781	2	AAE22050 pSOD/c200
23	1623	36.4	781	2	AAE22050 pSOD/c200
24	1623	36.4	781	2	AAE22050 pSOD/c200
25	1623	36.4	781	2	AAE22050 pSOD/c200

26	1623	36.4	781	4	AAE22050 pSOD/c200
27	1622.5	36.4	3011	5	AAU84597 HCV polyp
28	1621.5	36.4	2301	1	AAE22050 pSOD/c200
29	1621.5	36.4	2772	2	AAE22050 pSOD/c200
30	1619.5	36.4	2894	2	AAE22050 pSOD/c200
31	1616.5	36.3	2816	2	AAE22050 pSOD/c200
32	1615.5	36.3	2435	2	AAE22050 pSOD/c200
33	1614.5	36.2	2894	2	AAE22050 pSOD/c200
34	1614.5	36.2	3011	2	AAE22050 pSOD/c200
35	1608.5	36.1	2436	2	AAE22050 pSOD/c200
36	1605.5	36.0	1786	1	AAE22050 pSOD/c200
37	1600.5	35.9	2955	2	AAE22050 pSOD/c200
38	1597.5	35.9	2202	6	AAE22050 pSOD/c200
39	1597.5	35.9	2631	6	AAE22050 pSOD/c200
40	1597.5	35.9	2984	4	AAE22050 pSOD/c200
41	1597.5	35.9	3011	2	AAE22050 pSOD/c200
42	1597.5	35.9	3011	2	AAE22050 pSOD/c200
43	1597.5	35.9	3011	2	AAE22050 pSOD/c200
44	1597.5	35.9	3011	2	AAE22050 pSOD/c200
45	1597.5	35.9	3011	2	AAE22050 pSOD/c200

ALIGNMENTS

RESULT 1	AAE18690	standard; protein; 829 AA.
XX	AAE18690;	
XX	17-MAY-2002	(first entry)
XX	Multiple epitope fusion antigen (MEFA) 12 protein.	
XX	Hepatitis C virus; NS3/4a antigen; multiple epitope fusion antigen;	
XX	HCV infection; MEFA 12 protein.	
XX	Undifferentiated.	
XX	Key	Location/Qualifiers
XX	Misc-difference 315	/note= "Encoded by ATG"
XX	Misc-difference 645	/note= "Encoded by GAG"
XX	Misc-difference 645	/note= "Encoded by GAG"
XX	MO200196875-A2.	
XX	20-DEC-2001.	
XX	14-JUN-2001; 2001MO-US019369.	
XX	15-JUN-2000; 2000US-0212082P.	
XX	02-APR-2001; 2001US-0280811P.	
XX	02-APR-2001; 2001US-0280867P.	
XX	(CHIR) CHIRON CORP.	
XX	Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;	
XX	Medina-Selby A;	
XX	WPI; 2002-179522/23.	
XX	N-PSDB; AAD29796.	
XX	Immunosay solid support useful for detecting hepatitis C virus	
XX	infection in a biological sample, comprises at least one of HCV anti-core	
XX	antibody and HCV NS3/4a epitope, bound to the support.	
XX	Disclosure; Fig 7; 87pp; English.	
XX	The present invention relates to hepatitis C virus (HCV) core antigen and	
XX	NS (nonstructural) 3/4a antibody combination assay that can detect both	
XX	HCV antigens and antibodies present in a sample using a single solid	

SEQ ID NO:4

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OM protein - protein search, using SW model

Run on: June 21, 2004, 10:18:09 ; Search time 65.5868 Seconds
(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-6

Perfect score: 5912
Sequence: 1 MATKAVCVLKGDPVQGIIN.....GNKDRRSTGKSWKPGYPMW 1099

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneeqp1980s.*
2: geneeqp1990s.*
3: geneeqp2000s.*
4: geneeqp2001s.*
5: geneeqp2002s.*
6: geneeqp2003as.*
7: geneeqp2003bs.*
8: geneeqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	5912	100.0	1099	5	AAU76378
2	5912	100.0	1099	6	ABG72262 HCV multi
3	4032	68.2	829	5	AAE18690 Multiple
4	4032	68.2	829	7	ADCO6769 Chimeric
5	3829.5	64.8	1021	2	AAW34481 HCV anti
6	3829.5	64.8	1021	2	AAW40039 Fusion pr
7	3829.5	64.8	1021	5	AAE22050 pSOD/c200
8	3050.5	51.6	841	2	AAE68547 HCV prote
9	3050.5	51.6	841	6	ABO27020 Hepatitis
10	3050.5	51.6	841	7	ADA07875 HCV prote
11	3047.5	51.5	841	2	AAW01701 hSOD-HCV
12	3047.5	51.5	841	2	AAW46397 Anti
13	3047.5	51.5	841	2	AAW97609 Anti
14	3042.5	51.5	840	2	AAE14349 HCV prote
15	2909.5	49.2	2261	1	AAE90164 Peptide e
16	2909.5	49.2	2436	1	AAE92050 Sequence
17	2909.5	49.2	2436	1	AAE92050 Sequence
18	2909.5	49.2	2436	1	AAE92050 Sequence
19	2909.5	49.2	2436	1	AAE92050 Sequence
20	2909.5	49.2	2436	1	AAE92050 Sequence
21	2909.5	49.2	2436	1	AAE92050 Sequence
22	2909.5	49.2	2436	1	AAE92050 Sequence
23	2909.5	49.2	2436	1	AAE92050 Sequence
24	2909.5	49.2	2436	1	AAE92050 Sequence
25	2906.5	49.2	2301	1	AAE92047 Sequence

26	2906.5	49.2	2772	2	AAE08123	AAE08123 Hepatitis
27	2900.5	49.1	3011	5	AAE08123	AAE08123 Hepatitis
28	2900.5	49.1	3011	5	AAE08123	AAE08123 Hepatitis
29	2897.5	49.0	1766	1	AAE25135	AAE25135 HCV poly
30	2896.5	49.0	1766	1	AAE25135	AAE25135 HCV poly
31	2895.5	48.9	2894	2	AAE24440	AAE24440 Hepatitis
32	2893.5	48.9	2894	2	AAE24440	AAE24440 Hepatitis
33	2891.5	48.9	3011	2	AAE31621	AAE31621 HCV-1 pol
34	2890.5	48.9	1786	1	AAE90158	AAE90158 Protein s
35	2890.5	48.9	2894	2	AAE70230	AAE70230 Composite
36	2880.5	48.8	2436	2	AAE28582	AAE28582 HCV amino
37	2880.5	48.7	2955	2	AAE08124	AAE08124 Hepatitis
38	2877.5	48.7	3011	5	AAE2052	AAE2052 Hepatitis
39	2875	48.6	3011	2	AAE77397	AAE77397 Hepatitis
40	2875	48.6	3011	6	ABP71460	ABP71460 Anti
41	2875	48.6	3012	5	AAU99289	AAU99289 Hepatitis
42	2875	48.6	3012	6	ABU61848	ABU61848 HCV H77 c
43	2868	48.5	2984	4	AAE00442	AAE00442 Hepatitis
44	2868	48.5	3011	2	AAE77398	AAE77398 Hepatitis
45	2868	48.5	3011	2	AAE98021	AAE98021 Infection

ALIGNMENTS

RESULT 1

AAU76378 standard; protein; 1099 AA.

AAU76378;

08-MAY-2002 (first entry)

HCV multiple epitope fusion antigen (MEFA) 7.1 protein sequence.

Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;

immunoassay solid support; multiple epitope fusion antigen; MEFA;

non-structural protein.

Hepatitis C virus.

Synthetic.

WO200196870-A2.

14-JUN-2001; 2001WO-05019156.

15-JUN-2000; 2000US-0212082P.

02-APR-2001; 2001US-0280867P.

02-APR-2001; 2001US-0280867P.

(CHIR) CHIRON CORP.

Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

Medina-Selby A.

WPI, 2002-090228/12.

N-PSDB; ABR15345.

Immunosay solid support, useful for detecting hepatitis C virus

infection in biological sample, comprises HCV NS3/4a conformational

epitope and multiple epitope fusion antigen bound to the support.

Claim 5; Fig 5; 92pp; English.

The present invention relates to a new immunoassay solid support

consisting essentially of at least one hepatitis C virus (HCV) NS3/4a

conformational epitope and a multiple epitope fusion antigen (MEFA),

bound to the support. The NS3/4a conformational epitope and/or MEFA

reacts specifically with anti-HCV antibodies present in a biological

sample from an HCV-infected individual. The immunoassay of the invention

is useful for detecting hepatitis C virus infection in a biological

SEE ID NO: 6

Sequence 1099 AA;

QY 1 MATAVCLTKGDGPVQGIINEEQKESNGPVKMGSIKGLTEGLGHFHEFGNTAGCTS 60
DQ 1 MATAVCLTKGDGPVQGIINEEQKESNGPVKMGSIKGLTEGLGHFHEFGNTAGCTS 60

QY 61 AGHFNPLSRKHGGKDEERHVGDLNVTADKGVADVSIEDSVISLGGDHCIIGRTLVV 120
 D6 61 AGHFNPLSRKHGGKDEERHVGDLNVTADKGVADVSIEDSVISLGGDHCIIGRTLVV 120

QY 121 HEKADDLGKGNESSTKTGNAGSRLLACGVITGIAQNLNSGCNCSITYPGHITGHRMAWKLG 180
 Dp 121 HEKADDLGKGNESSTKTGNAGSRLLACGVITGIAQNLNSGCNCSITYPGHITGHRMAWKLG 180

Db

181 AARTTSGFVSLFAPGAKONHTHTGGAARITTSGLTSLFSPGASONQLIVDFIVENLE 240

241 TTKRSPVFTDNGSPVVFQFVAHLHAPGSGSKTKVPAAVAAQGIKVLVLPVSAATL 300

Dd 301 GFGAYMSRAHGIDPNIRKTVRTITGSPITYSTYGNFLADGGCCSGAYDIIICDECHSTD 360

Db 361 AASILGISTVLDQAEIAGARLVLTATATPPGASVTVPHNIEVALSTGEIIPFYGA1PL 420

421 EITKGRRLIFCHSKKKCDLAAKVALGINAVAYRGLDVSVIPISGDVVAVATDALMT 480

481 GTTGDFSVIDCMTCVTQTWDFSLDPTFTTETITLPQDAVSRTQRRGRTGKPKGIYRFV 540

541 APERPSGWFDSVLCCEYDAGCMYELTPAETTRLRAYNNTPLGLVCCQHLFEFMEGVF 600

661 TGLTHIDAHFLSQTKSGENLPYLVAYQATVCARAQAPPSWDQMWKCLIRLKPFLHGPT 660

661 PLYRLGAVQNEITLTHTPEVTKYIMTCSADLEVVTSA CSGKPAILPDREVAIREFDEMEE 720

721 CSQHLPTIEGMMLEAGFQKALGSRGKRALVPDKETLYQQYDEMECCQAAPYTEQA 780

QY	781	VIAHOFEXKLTGLINDQVVVTPDKELTYAFDMECASQAALIESQMAEMLKSTI	840
Db	781	QVIAHOFEXKLTGLINDQVVVTPDKELTYAFDMECASQAALIESQMAEMLKSTI	840
QY	841	QGLIGILRBHVPGEQAVOMNNRLIAPASRGNHSPTYVBSRSRFRQALPVMARPDYN	900
Db	841	QGLIGILRBHVPGEQAVOMNNRLIAPASRGNHSPTYVBSRSRFRQALPVMARPDYN	900
QY	901	PLVETWKKPDYEPBPVVGHRSSRRFAQALPVMARPDYNPLVETWKKPDYEPBVHGRXT	960
Db	901	PLVETWKKPDYEPBPVVGHRSSRRFAQALPVMARPDYNPLVETWKKPDYEPBVHGRXT	960
QY	961	KRANTRRBPQVYKPPGGQIVGRGPPPIPKARRPESGRTWAOGYPMPLIGNDKRSTGKSM	102
Db	961	KRANTRRBPQVYKPPGGQIVGRGPPPIPKARRPESGRTWAOGYPMPLIGNDKRSTGKSM	102
QY	1021	GKPGYPMPRKTKRNTNRRPQDVYKPPGGQIVGRGPPPIPKARRPESGRTWAOGYPMPLYG	108
Db	1021	GKPGYPMPRKTKRNTNRRPQDVYKPPGGQIVGRGPPPIPKARRPESGRTWAOGYPMPLYG	108
QY	1081	NKDRSTGKSMGKPGYPM 1099	
Db	1081	NKDRSTGKSMGKPGYPM 1099	

RESULT 2
ABG72262
ID ABG72262 standard; protein; 1099 AA

AC	ABG72262;	
XX		
DT	06-MAR-2003	(first entry)
XY		

DE HCV multiple epitope fusion antigen 7.1 (MEPA 7.1).
XX
KM Immunoassay solid support; Hepatitis C Virus type-1; HCV-1;
KM NS3/4a conformational epitope, multiple epitope fusion antigen 7.1,
KM MEPA 7.1; anti-HCV antibody; NS3/4a conformational antigen; HCV-3;
KM HCV infection; Hepatitis C Virus type-2; Hepatitis C Virus type-3;
KM mutant; mutin.

05	Hepatitis C virus type 1.
05	Hepatitis C virus type 2.
05	Hepatitis C virus type 3.
05	Synthetic.
05	Chimeric.

EH	Key
ET	Rec

ET

ET ET

ET

ET

Reg
ET

FT Rec

~~ET~~
~~Reo~~

~~SECRET~~

ET

Key
LT

Location/Qualifiers
1..156
/note= "Correspond to amino acids 1-156 of HCV-1 h50D superoxide dismutase)"
159..176
/note= "Correspond to amino acids 303-320 of HCV-1 E1"
179..199
/note= "Correspond to consensus sequence of amino acids 390-410 of HCV-1 E2 HVR"
200..230
/note= "Correspond to consensus sequence of amino acids 384-414 of HCV-1 and HCV-2 E2 HVR"
231..696
/note= "Correspond to amino acids 1193-1658 of HCV-1 helicase"
699..745
/note= "Correspond to amino acids 1689-1735 of HCV-1 1 epitope"
748..794
/note= "Correspond to amino acids 1689-1735 of HCV-3 5-1 1 epitope"
797..843
/note= "Correspond to amino acids 1689-1735 of HCV-2 5-1 1 epitope"
846..881
/note= "Correspond to amino acids 1901-1936 of HCV-1